HIGH-RESOLUTION RECOMBINATION DISSECTION AROUND ALIEN CHROMOSOME SEGMENTS CONTAINING GENES FOR RESISTANCE TO RENIFORM NEMATODES

Xiuting Zheng Fei Wang Texas A&M University **College Station**, TX Jose Ouintana USDA-ARS-SPARC **College Station, TX** Hamid Ashrafi **University of California-Davis** Davis, CA David M. Stelly Texas A&M University **College Station**, TX Alois A. Bell **USDA-ARS-SPARC College Station, TX** Allen Van Devnze **University of California-Davis** Davis, CA **Don Jones Robert L. Nichols Cotton Incorporated** Carv, NC

<u>Abstract</u>

Reniform (Rotylenchulus reniformis) nematodes are plant pathogens with a wide host range and wide global distribution. They cost the US over \$130M per year in lost cotton yield, guality and other expenses. In previous work, we introgressed the resistance trait by hybridizing the African diploid with a synthetic hexaploid $(2([AD]_1D_2))$ 1)) "bridge" to create a tetraploid $[AD]_1D_{2-1}F_1$ tri-species hybrid. We also identified the resistance locus, Ren^{lon}, and derived highly resistant lines LONREN 1 and LONREN 2. Collaborative field-testing of the lines revealed variable levels of "stunting" in "reniform-hot" fields. Such stunting could be due to hypersensitivity and/or a modified pathogen resistance profile, such as might arise from loss of Upland cotton soil pathogen resistance genes when replaced by the alien segment. Accordingly, we have mounted a marker-assisted selection (MAS) breeding approach to combine Ren^{lon} with flanking Upland cotton segments by identifying rare double-recombinants very close to *Ren^{lon}*, since these will prospectively be both nematode-resistant and free of stunting. We have created populations of testcross seed (10.000s) to recover the rare double recombinants, and also developed large numbers (10.000s) of markers (SSRs and SNPs) in this region of chromosome 11. After determining which markers are in the region of interest, we will use them to identify and order the recombination events according to relative position. The most closely flanking recombinants will be biologically tested for resistance and/or agronomic performance. When completed, this work [1] will provide insight into the cause of "stunting", [2] may render the Renlon gene into a very valuable resource for cotton breeding and [3] enable MAS breeding in a chromosome segment that is replete with valuable resistance, agronomic and fiber traits.